CRF Error Corrected by the STIC Systems Branch

Serial Number: _09/684,215A_ ~~CRF~~

ENTERED

CRF Processing Date: _4/16/2002_
Edited by: _____
Verified by: _____ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.

☐ Edited a format error in the Current Application Data section, specifically: _____

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____

☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included: _____

☐ Deleted extra, invalid, headings used by an applicant, specifically: _____

☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as_____.

☑ Inserted mandatory headings, specifically: _<2207 globally_

☐ Corrected an obvious error in the response, specifically: _____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically: _____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____

☐ Other: _____
_____
_____

*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING   DATE: 04/16/2002
PATENT APPLICATION: US/09/684,215A   TIME: 09:31:03

Input Set : A:\-80-1.app
Output Set: N:\CRF3\04162002\I684215A.raw

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252 65                    70                  75                  80
254 atc acc gcg gtc gac ggc gct ccg atc aac tcg gcc acc gcg atg gcg   288
255 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
256                85                  90                  95
258 gac gcg ctt aac ggg cat cat ccc ggt gac gtc atc tcg gtg acc tgg   336
259 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
260         100                 105                 110
262 caa acc aag tcg ggc ggc acg cgt aca ggg aac gtg aca ttg gcc gag   384
263 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
264         115                 120                 125
266 gga ccc ccg gcc                                                   396
267 Gly Pro Pro Ala
268     130
271 <210> SEQ ID NO: 4
272 <211> LENGTH: 132
273 <212> TYPE: PRT
274 <213> ORGANISM: Mycobacterium tuberculosis                      〉〈2207
275 <223> OTHER INFORMATION: 14 KD C-terminal fragment of MTB32A Ra12
277 <400> SEQUENCE: 4
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279   1               5                  10                  15
280 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
281                20                  25                  30
282 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
283         35                  40                  45
284 Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
285     50                  55                  60
286 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
287  65                  70                  75                  80
288 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
289                85                  90                  95
290 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
291         100                 105                 110
292 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
293         115                 120                 125
294 Gly Pro Pro Ala
295     130
298 <210> SEQ ID NO: 5
299 <211> LENGTH: 702
300 <212> TYPE: DNA
301 <213> ORGANISM: Artificial Sequence
303 <220> FEATURE:
304 <221> NAME/KEY: CDS
305 <222> LOCATION: (4)..(696)
306 <223> OTHER INFORMATION: Ra12-DPPD fusion polypeptide
308 <220> FEATURE:
309 <223> OTHER INFORMATION: Description of Artificial Sequence:Ra12-DPPD fusion
310 ,       polypeptide
312 <400> SEQUENCE: 5
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1600

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 3 <110> APPLICANT: Skeiky, Yasir
 4         Guderian, Jeffrey
 5         Corixa Corporation
 7 <120> TITLE OF INVENTION: Methods of Using a Mycobacterium tuberculosis Coding
 8         Sequence to Facilitate Stable and High Yield Expression
 9         of Heterologous Proteins
11 <130> FILE REFERENCE: 014058-008010US
13 <140> CURRENT APPLICATION NUMBER: US 09/684,215A
14 <141> CURRENT FILING DATE: 2000-10-06
16 <150> PRIOR APPLICATION NUMBER: US 60/158,585
17 <151> PRIOR FILING DATE: 1999-10-07
19 <160> NUMBER OF SEQ ID NOS: 22
21 <170> SOFTWARE: PatentIn Ver. 2.1
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 1872
25 <212> TYPE: DNA
26 <213> ORGANISM: Mycobacterium tuberculosis
28 <220> FEATURE:
29 <223> OTHER INFORMATION: 32 KD serine protease MTB32A
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (89)..(1156)
34 <223> OTHER INFORMATION: MTB32A
36 <220> FEATURE:
37 <221> NAME/KEY: sig_peptide
38 <222> LOCATION: (89)..(184)
39 <223> OTHER INFORMATION: N-terminal hydrophobic secretory signal sequence
41 <220> FEATURE:
42 <221> NAME/KEY: mat_peptide
43 <222> LOCATION: (185)..(1153)
45 <400> SEQUENCE: 1
46 gactacgttg gtgtagaaaa atcctgccgc ccggaccctt aaggctggga caatttctga 60
48 tagctacccc gacacaggag gttacggg atg agc aat tcg cgc cgc cgc tca     112
49                                 Met Ser Asn Ser Arg Arg Arg Ser
50                                     -30                 -25
52 ctc agg tgg tca tgg ttg ctg agc gtg ctg gct gcc gtc ggg ctg ggc   160
53 Leu Arg Trp Ser Trp Leu Leu Ser Val Leu Ala Ala Val Gly Leu Gly
54             -20             -15                 -10
56 ctg gcc acg gcg ccg gcc cag gcg gcc ccg ccg gcc ttg tcg cag gac   208
57 Leu Ala Thr Ala Pro Ala Gln Ala Ala Pro Pro Ala Leu Ser Gln Asp
58             -5              -1  1               5
60 cgg ttc gcc gac ttc ccc gcg ctg ccc ctc gac ccg tcc gcg atg gtc   256
61 Arg Phe Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val
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RAW SEQUENCE LISTING   DATE: 04/16/2002
PATENT APPLICATION: US/09/684,215A   TIME: 11:24:16

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\04162002\I684215A.raw

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62     10                    15                    20
64 gcc caa gtg ggg cca cag gtg gtc aac atc aac acc aaa ctg ggc tac    304
65 Ala Gln Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr
66  25              30                    35                    40
68 aac aac gcc gtg ggc gcc ggg acc ggc atc gtc atc gat ccc aac ggt    352
69 Asn Asn Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly
70                  45                    50                    55
72 gtc gtg ctg acc aac aac cac gtg atc gcg ggc gcc acc gac atc aat    400
73 Val Val Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn
74              60                    65                    70
76 gcg ttc agc gtc ggc tcc ggc caa acc tac ggc gtc gat gtg gtc ggg    448
77 Ala Phe Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly
78          75                    80                    85
80 tat gac cgc acc cag gat gtc gcg gtg ctg cag ctg cgc ggt gcc ggt    496
81 Tyr Asp Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly
82      90                    95                    100
84 ggc ctg ccg tcg gcg gcg atc ggt ggc ggc gtc gcg gtt ggt gag ccc    544
85 Gly Leu Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro
86 105              110                    115                    120
88 gtc gtc gcg atg ggc aac agc ggt ggg cag ggc gga acg ccc cgt gcg    592
89 Val Val Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala
90                  125                    130                    135
92 gtg cct ggc agg gtg gtc gcg ctc ggc caa acc gtg cag gcg tcg gat    640
93 Val Pro Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp
94              140                    145                    150
96 tcg ctg acc ggt gcc gaa gag aca ttg aac ggg ttg atc cag ttc gat    688
97 Ser Leu Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp
98          155                    160                    165
100 gcc gcg atc cag ccc ggt gat tcg ggc ggg ccc gtc gtc aac ggc cta   736
101 Ala Ala Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu
102     170                    175                    180
104 gga cag gtg gtc ggt atg aac acg gcc gcg tcc gat aac ttc cag ctg   784
105 Gly Gln Val Val Gly Met Asn Thr Ala Ala Ser Asp Asn Phe Gln Leu
106 185                    190                    195                    200
108 tcc cag ggt ggg cag gga ttc gcc att ccg atc ggg cag gcg atg gcg   832
109 Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala
110                  205                    210                    215
112 atc gcg ggc cag atc cga tcg ggt ggg ggg tca ccc acc gtt cat atc   880
113 Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile
114                  220                    225                    230
116 ggg cct acc gcc ttc ctc ggc ttg ggt gtt gtc gac aac aac ggc aac   928
117 Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn
118              235                    240                    245
120 ggc gca cga gtc caa cgc gtg gtc ggg agc gct ccg gcg gca agt ctc   976
121 Gly Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu
122     250                    255                    260
124 ggc atc tcc acc ggc gac gtg atc acc gcg gtc gac ggc gct ccg atc  1024
125 Gly Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile
126 265                    270                    275                    280
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RAW SEQUENCE LISTING   DATE: 04/16/2002
PATENT APPLICATION: US/09/684,215A   TIME: 11:24:16

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF3\04162002\I684215A.raw

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128 aac tcg gcc acc gcg atg gcg gac gcg ctt aac ggg cat cat ccc ggt   1072
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130             285             290             295
132 gac gtc atc tcg gtg acc tgg caa acc aag tcg ggc ggc acg cgt aca   1120
133 Asp Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr
134             300             305             310
136 ggg aac gtg aca ttg gcc gag gga ccc ccg gcc tga tttcgtcgcg        1166
137 Gly Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
138             315             320
140 gataccaccc gccggccggc caattggatt ggcgccagcc gtgattgccg cgtgagcccc 1226
142 cgagttccgt ctcccgtgcg cgtggcatcg tggaagcaat gaacgaggca gaacacagcg 1286
144 tcgagcaccc tcccgtgcag ggcagtcacg tcgaaggcgg tgtggtcgag catccggatg 1346
146 ccaaggactt cggcagcgcc gccgccctgc ccgccgatcc gacctggttt aagcacgccg 1406
148 tcttctacga ggtgctggtc cgggcgttct tcgacgccag cgcggacggt tccggcgatc 1466
150 tgcgtggact catcgatcgc ctcgactacc tgcagtggct tggcatcgac tgcatctggt 1526
152 tgccgccgtt ctacgactcg ccgctgcgcg acggcggtta cgacattcgc gacttctaca 1586
154 aggtgctgcc cgaattcggc accgtcgacg atttcgtcgc cctggtcgac gccgctcacc 1646
156 ggcgaggtat ccgcatcatc accgacctgg tgatgaatca cacctcggag tcgcacccct 1706
158 ggtttcagga gtcccgccgc gacccagacg gaccgtacgg tgactattac gtgtggagcg 1766
160 acaccagcga gcgctacacc gacgcccgga tcatcttcgt cgacaccgaa gagtcgaact 1826
162 ggtcattcga tcctgtccgc cgacagttct actggcaccg attctt            1872
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166 <211> LENGTH: 355
167 <212> TYPE: PRT
168 <213> ORGANISM: Mycobacterium tuberculosis
170 <220> FEATURE:
171 <223> OTHER INFORMATION: 32 KD serine protease MTB32A
173 <400> SEQUENCE: 2
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175  1               5               10              15
176 Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala
177             20              25              30
178 Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
179         35              40              45
180 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val Val
181     50              55              60
182 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
183 65              70              75              80
184 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
185             85              90              95
186 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
187             100             105             110
188 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
189         115             120             125
190 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
191     130             135             140
192 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
193 145             150             155             160
194 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
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195                   165                 170                   175
196 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
197             180                 185                   190
198 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
199         195                 200                   205
200 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
201     210                 215                   220
202 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
203 225                 230                   235                   240
204 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
205             245                 250                   255
206 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
207             260                 265                   270
208 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
209         275                 280                   285
210 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
211     290                 295                   300
212 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
213 305             310                 315                   320
214 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp Gln
215             325                 330                   335
216 Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
217         340                 345                   350
218 Pro Pro Ala
219         355
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223 <211> LENGTH: 396
224 <212> TYPE: DNA
225 <213> ORGANISM: Mycobacterium tuberculosis
227 <220> FEATURE:
228 <223> OTHER INFORMATION: 14 KD C-terminal fragment of MTB32A Ra12
230 <220> FEATURE:
231 <221> NAME/KEY: CDS
232 <222> LOCATION: (1)..(396)
233 <223> OTHER INFORMATION: Ra12
235 <400> SEQUENCE: 3
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238  1               5                   10                  15
240 gcc att ccg atc ggg cag gcg atg gcg atc gcg ggc cag atc cga tcg   96
241 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
242             20                  25                  30
244 ggt ggg ggg tca ccc acc gtt cat atc ggg cct acc gcc ttc ctc ggc  144
245 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
246         35                  40                  45
248 ttg ggt gtt gtc gac aac aac ggc aac ggc gca cga gtc caa cgc gtg  192
249 Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
250     50                  55                  60
252 gtc ggg agc gct ccg gcg gca agt ctc ggc atc tcc acc ggc gac gtg  240
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253 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
254  65                  70                  75                  80
256 atc acc gcg gtc gac ggc gct ccg atc aac tcg gcc acc gcg atg gcg   288
257 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
258                  85                  90                  95
260 gac gcg ctt aac ggg cat cat ccc ggt gac gtc atc tcg gtg acc tgg   336
261 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
262             100                 105                 110
264 caa acc aag tcg ggc ggc acg cgt aca ggg aac gtg aca ttg gcc gag   384
265 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
266          115                 120                 125
268 gga ccc ccg gcc                                                   396
269 Gly Pro Pro Ala
270      130
273 <210> SEQ ID NO: 4
274 <211> LENGTH: 132
275 <212> TYPE: PRT
276 <213> ORGANISM: Mycobacterium tuberculosis
278 <220> FEATURE:
279 <223> OTHER INFORMATION: 14 KD C-terminal fragment of MTB32A Ra12
281 <400> SEQUENCE: 4
282 Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
283   1               5                  10                  15
284 Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
285             20                  25                  30
286 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
287          35                  40                  45
288 Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
289      50                  55                  60
290 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
291  65                  70                  75                  80
292 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
293                  85                  90                  95
294 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Thr Trp
295             100                 105                 110
296 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
297          115                 120                 125
298 Gly Pro Pro Ala
299      130
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303 <211> LENGTH: 702
304 <212> TYPE: DNA
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <221> NAME/KEY: CDS
309 <222> LOCATION: (4)..(696)
310 <223> OTHER INFORMATION: Ra12-DPPD fusion polypeptide
312 <220> FEATURE:
313 <223> OTHER INFORMATION: Description of Artificial Sequence:Ra12-DPPD fusion
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VERIFICATION SUMMARY   DATE: 04/16/2002
PATENT APPLICATION: US/09/684,215A   TIME: 11:24:17

Input Set : **A:\PTO.AMC.txt**
Output Set: **N:\CRF3\04162002\I684215A.raw**